

10/580906

AP20 Rec'd PCT/PTO 26 MAY 2006

SEQUENCE LISTING

<110> FUKATSU et al.

<120> RECEPTOR FUNCTION REGULATING AGENT

<130> 20039.0005USWO

<140> New Filing

<141> 2006-05-26

<150> PCT/JP2004/017996

<151> 2004-11-26

<150> JP 2003-394848

<151> 2003-11-26

<160> 20

<170> PatentIn Version 3.1

<210> 1

<211> 361

<212> PRT

<213> Human

<400> 1

```

Met Ser Pro Glu Cys Ala Arg Ala Ala Gly Asp Ala Pro Leu Arg Ser
      5              10              15
Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys
      20              25              30
Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val
      35              40              45
Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
      50              55              60
Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn
      65              70              75              80
Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu
      85              90              95
Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His
      100             105             110
Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr
      115             120             125
Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln
      130             135             140
Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala
      145             150             155             160
Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe
      165             170             175
Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser
      180             185             190
Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp
      195             200             205
Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
      210             215             220
Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
      225             230             235             240

```

Leu	Thr	Val	Ser	Leu	Ala	Tyr	Ser	Glu	Ser	His	Gln	Ile	Arg	Val	Ser
				245					250					255	
Gln	Gln	Asp	Phe	Arg	Leu	Phe	Arg	Thr	Leu	Phe	Leu	Leu	Met	Val	Ser
			260					265					270		
Phe	Phe	Ile	Met	Trp	Ser	Pro	Ile	Ile	Ile	Thr	Ile	Leu	Leu	Ile	Leu
		275					280				285				
Ile	Gln	Asn	Phe	Lys	Gln	Asp	Leu	Val	Ile	Trp	Pro	Ser	Leu	Phe	Phe
	290					295					300				
Trp	Val	Val	Ala	Phe	Thr	Phe	Ala	Asn	Ser	Ala	Leu	Asn	Pro	Ile	Leu
305					310					315					320
Tyr	Asn	Met	Thr	Leu	Cys	Arg	Asn	Glu	Trp	Lys	Lys	Ile	Phe	Cys	Cys
				325					330					335	
Phe	Trp	Phe	Pro	Glu	Lys	Gly	Ala	Ile	Leu	Thr	Asp	Thr	Ser	Val	Lys
			340					345					350		
Arg	Asn	Asp	Leu	Ser	Ile	Ile	Ser	Gly							
		355					360								

<210> 2

<211> 1083

<212> DNA

<213> Human

<400> 2

atgtcccctg	aatgcgcgcg	ggcagcgggc	gacgcgccct	tgcgcagcct	ggagcaagcc	60
aaccgcaccc	gctttccctt	cttctccgac	gtcaagggcg	accaccggct	ggtgctggcc	120
gcggtggaga	caaccgtgct	ggtgctcatc	tttgcagtgt	cgctgctggg	caacgtgtgc	180
gccctggtgc	tgggtggcgcg	ccgacgacgc	cgcggcgcga	ctgcctgcct	ggtactcaac	240
ctcttctgcg	cggacctgct	cttcatcagc	gctatccctc	tgggtgctggc	cgtgcgctgg	300
actgaggect	ggctgctggg	ccccgttgcc	tgccacctgc	tcttctacgt	gatgaccctg	360
agcggcagcg	tcaccatcct	cacgctggcc	gcggtcagcc	tggagcgcac	ggtgtgcatc	420
gtgcacctgc	agcgcggcgt	gcggggctct	ggcgggcggg	cgcgggcagt	gctgctggcg	480
ctcatctggg	gctattcggc	ggtcgccgct	ctgcctctct	gcgtcttctt	ccgagtcgct	540
ccgcaacggc	tccccggcgc	cgaccaggaa	atttcgattt	gcacactgat	ttggcccacc	600
attcctggag	agatctcgtg	ggatgtctct	tttgttactt	tgaacttctt	ggtgccagga	660
ctggtcattg	tgatcagtta	ctccaaaatt	ttacagatca	caaaggcatc	aaggaagagg	720
ctcacggtaa	gcctggccta	ctcgagagac	caccagatcc	gcgtgtccca	gcaggacttc	780
cggctcttcc	gcacctctct	cctcctcatg	gtctccttct	tcatcatgtg	gagccccatc	840
atcatcacca	tcctcctcat	cctgatccag	aacttcaagc	aagacctggg	catctggccg	900
tcctcttctt	tctgggtggg	ggccttcaca	tttgctaatt	cagccctaaa	ccccatcctc	960
tacaacatga	cactgtgcag	gaatgagtgg	aagaaaattt	tttgctgctt	ctggttccca	1020
gaaaaggagg	ccattttaac	agacacatct	gtcaaaagaa	atgacttgct	gattatttct	1080
ggc						1083

<210> 3

<211> 361

<212> PRT

<213> Mouse

<400> 3

Met	Ser	Pro	Glu	Cys	Ala	Gln	Thr	Thr	Gly	Pro	Gly	Pro	Ser	His	Thr
				5					10					15	
Leu	Asp	Gln	Val	Asn	Arg	Thr	His	Phe	Pro	Phe	Phe	Ser	Asp	Val	Lys
			20					25					30		
Gly	Asp	His	Arg	Leu	Val	Leu	Ser	Val	Val	Glu	Thr	Thr	Val	Leu	Gly
		35					40					45			
Leu	Ile	Phe	Val	Val	Ser	Leu	Leu	Gly	Asn	Val	Cys	Ala	Leu	Val	Leu
	50					55					60				
Val	Ala	Arg	Arg	Arg	Arg	Arg	Gly	Ala	Thr	Ala	Ser	Leu	Val	Leu	Asn
	65				70					75					80
Leu	Phe	Cys	Ala	Asp	Leu	Leu	Phe	Thr	Ser	Ala	Ile	Pro	Leu	Val	Leu
				85					90					95	

Val	Val	Arg	Trp	Thr	Glu	Ala	Trp	Leu	Leu	Gly	Pro	Val	Val	Cys	His
			100					105					110		
Leu	Leu	Phe	Tyr	Val	Met	Thr	Met	Ser	Gly	Ser	Val	Thr	Ile	Leu	Thr
		115					120					125			
Leu	Ala	Ala	Val	Ser	Leu	Glu	Arg	Met	Val	Cys	Ile	Val	Arg	Leu	Arg
	130					135					140				
Arg	Gly	Leu	Ser	Gly	Pro	Gly	Arg	Arg	Thr	Gln	Ala	Ala	Leu	Leu	Ala
145					150					155					160
Phe	Ile	Trp	Gly	Tyr	Ser	Ala	Leu	Ala	Ala	Leu	Pro	Leu	Cys	Ile	Leu
			165						170					175	
Phe	Arg	Val	Val	Pro	Gln	Arg	Leu	Pro	Gly	Gly	Asp	Gln	Glu	Ile	Pro
		180						185					190		
Ile	Cys	Thr	Leu	Asp	Trp	Pro	Asn	Arg	Ile	Gly	Glu	Ile	Ser	Trp	Asp
	195						200					205			
Val	Phe	Phe	Val	Thr	Leu	Asn	Phe	Leu	Val	Pro	Gly	Leu	Val	Ile	Val
	210					215					220				
Ile	Ser	Tyr	Ser	Lys	Ile	Leu	Gln	Ile	Thr	Lys	Ala	Ser	Arg	Lys	Arg
225				230						235					240
Leu	Thr	Leu	Ser	Leu	Ala	Tyr	Ser	Glu	Ser	His	Gln	Ile	Arg	Val	Ser
			245					250						255	
Gln	Gln	Asp	Tyr	Arg	Leu	Phe	Arg	Thr	Leu	Phe	Leu	Leu	Met	Val	Ser
		260					265						270		
Phe	Phe	Ile	Met	Trp	Ser	Pro	Ile	Ile	Ile	Thr	Ile	Leu	Leu	Ile	Leu
	275						280					285			
Ile	Gln	Asn	Phe	Arg	Gln	Asp	Leu	Val	Ile	Trp	Pro	Ser	Leu	Phe	Phe
	290				295						300				
Trp	Val	Val	Ala	Phe	Thr	Phe	Ala	Asn	Ser	Ala	Leu	Asn	Pro	Ile	Leu
305				310						315					320
Tyr	Asn	Met	Ser	Leu	Phe	Arg	Asn	Glu	Trp	Arg	Lys	Ile	Phe	Cys	Cys
			325					330						335	
Phe	Phe	Phe	Pro	Glu	Lys	Gly	Ala	Ile	Phe	Thr	Asp	Thr	Ser	Val	Arg
		340						345					350		
Arg	Asn	Asp	Leu	Ser	Val	Ile	Ser	Ser							
	355						360								

<210> 4

<211> 1083

<212> DNA

<213> Mouse

<400> 4

atgtcccctg	agtgtgcaca	gacgacgggc	cctggcccct	cgcacaccct	ggaccaagtc	60
aatcgacccc	acttcccttt	cttctcggat	gtcaaggcg	accaccggtt	ggtgttgagc	120
gtcgtggaga	ccaccgttct	ggggctcatc	tttgtcgtct	cactgctggg	caacgtgtgt	180
gctctagtgc	tgggtggcgcg	ccgtcggcgc	cgtggggcga	cagccagcct	ggtgctcaac	240
ctcttctgcg	cggatttgct	cttcaccagc	gccatccctc	tagtgctcgt	cgtgcgctgg	300
actgaggcct	ggctgttggg	gcccgtcgtc	tgccacctgc	tcttctacgt	gatgacaatg	360
agcggcagcg	tcacgatcct	cacactggcc	gcggtcagcc	tggagcgcgt	ggtgtgcatc	420
gtgcgcctcc	ggcgcggctt	gagcggcccg	gggcggcgga	ctcaggcggc	actgctggct	480
ttcatatggg	gttactcggc	gctcgcgcgc	ctgcccctct	gcatcttggt	ccgcgtggtc	540
ccgcagcgcc	ttcccggcgc	ggaccaggaa	attccgattt	gcacattgga	ttggcccaac	600
cgcataggag	aaatctcatg	ggatgtgttt	tttgtgactt	tgaacttcct	ggtgccggga	660
ctggctcattg	tgatcagtta	ctccaaaatt	ttacagatca	cgaaagcatc	gcggaagagg	720
cttacgctga	gcttggcata	ctctgagagc	caccagatcc	gagtgtccca	acaagactac	780
cgactcttcc	gcacgctctt	cctgctcatg	gtttccttct	tcatcatgtg	gagtcccatc	840
atcatcacca	tcctcctcat	cttgatccaa	aacttcgggc	aggacctggt	catctggcca	900
tcccttttct	tctgggtggg	ggccttcacg	tttgccaaact	ctgccctaaa	ccccatactg	960
tacaacatgt	cgctgttcag	gaacgaatgg	aggaagattt	tttgctgctt	cttttttcca	1020
gagaaggagg	ccattttttac	agacacgtct	gtcaggcgaa	atgacttgct	tgttatttcc	1080

agc

1083

<210> 5

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<400> 5

gctgtggcat gcttttaaac 20

<210> 6

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<400> 6

cgctgtggat gtctatttgc 20

<210> 7

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<400> 7

agttcatttc cagtaccctc catcagtggc 30

<210> 8

<211> 361

<212> PRT

<213> Rat

<400> 8

Met	Ser	Pro	Glu	Cys	Ala	Gln	Thr	Thr	Gly	Pro	Gly	Pro	Ser	Arg	Thr	
				5					10					15		
Pro	Asp	Gln	Val	Asn	Arg	Thr	His	Phe	Pro	Phe	Phe	Ser	Asp	Val	Lys	
			20					25					30			
Gly	Asp	His	Arg	Leu	Val	Leu	Ser	Val	Leu	Glu	Thr	Thr	Val	Leu	Gly	
		35					40					45				
Leu	Ile	Phe	Val	Val	Ser	Leu	Leu	Gly	Asn	Val	Cys	Ala	Leu	Val	Leu	
	50					55					60					
Val	Val	Arg	Arg	Arg	Arg	Arg	Gly	Ala	Thr	Val	Ser	Leu	Val	Leu	Asn	
	65				70					75					80	
Leu	Phe	Cys	Ala	Asp	Leu	Leu	Phe	Thr	Ser	Ala	Ile	Pro	Leu	Val	Leu	
				85					90					95		
Val	Val	Arg	Trp	Thr	Glu	Ala	Trp	Leu	Leu	Gly	Pro	Val	Val	Cys	His	
		100						105					110			
Leu	Leu	Phe	Tyr	Val	Met	Thr	Met	Ser	Gly	Ser	Val	Thr	Ile	Leu	Thr	
	115					120						125				
Leu	Ala	Ala	Val	Ser	Leu	Glu	Arg	Met	Val	Cys	Ile	Val	Arg	Leu	Arg	
	130					135					140					
Arg	Gly	Leu	Ser	Gly	Pro	Gly	Arg	Arg	Thr	Gln	Ala	Ala	Leu	Leu	Ala	
	145				150					155					160	
Phe	Ile	Trp	Gly	Tyr	Ser	Ala	Leu	Ala	Ala	Leu	Pro	Leu	Cys	Ile	Leu	
				165					170					175		
Phe	Arg	Val	Val	Pro	Gln	Arg	Leu	Pro	Gly	Gly	Asp	Gln	Glu	Ile	Pro	
		180					185						190			
Ile	Cys	Thr	Leu	Asp	Trp	Pro	Asn	Arg	Ile	Gly	Glu	Ile	Ser	Trp	Asp	
	195					200						205				
Val	Phe	Phe	Val	Thr	Leu	Asn	Phe	Leu	Val	Pro	Gly	Leu	Val	Ile	Val	
	210					215					220					
Ile	Ser	Tyr	Ser	Lys	Ile	Leu	Gln	Ile	Thr	Lys	Ala	Ser	Arg	Lys	Arg	
	225				230					235					240	

Leu	Thr	Leu	Ser	Leu	Ala	Tyr	Ser	Glu	Ser	His	Gln	Ile	Arg	Val	Ser
				245					250					255	
Gln	Gln	Asp	Tyr	Arg	Leu	Phe	Arg	Thr	Leu	Phe	Leu	Leu	Met	Val	Ser
			260					265					270		
Phe	Phe	Ile	Met	Trp	Ser	Pro	Ile	Ile	Ile	Thr	Ile	Leu	Leu	Ile	Leu
		275					280					285			
Ile	Gln	Asn	Phe	Arg	Gln	Asp	Leu	Val	Ile	Trp	Pro	Ser	Leu	Phe	Phe
	290					295					300				
Trp	Val	Val	Ala	Phe	Thr	Phe	Ala	Asn	Ser	Ala	Leu	Asn	Pro	Ile	Leu
	305				310					315					320
Tyr	Asn	Met	Ser	Leu	Phe	Arg	Ser	Glu	Trp	Arg	Lys	Ile	Phe	Cys	Cys
			325						330					335	
Phe	Phe	Phe	Pro	Glu	Lys	Gly	Ala	Ile	Phe	Thr	Glu	Thr	Ser	Ile	Arg
			340					345					350		
Arg	Asn	Asp	Leu	Ser	Val	Ile	Ser	Thr							
		355					360								

<210> 9

<211> 1083

<212> DNA

<213> Rat

<400> 9

atgtcccctg	agtgtgcgca	gacgacgggc	cctggcccct	cgcgcacccc	ggaccaagtc	60
aatcgacccc	acttcccttt	cttctcggat	gtcaagggcg	accaccggct	ggtgctgagc	120
gtcctggaga	ccaccgttct	gggactcatc	tttgtgggtc	cactgctggg	caacgtgtgt	180
gccctgggtg	tgggtgggtg	ccgtcggcgc	cgtggggcga	cagtcagctt	ggtgctcaac	240
ctcttctgcg	cggatttgct	cttcaccagc	gccatccctc	tagtgctcgt	ggtgcgctgg	300
actgaagcct	ggctgctggg	gcccgtcgtc	tgccacctgc	tcttctacgt	gatgaccatg	360
agcggcagcg	tcacgatcct	cacgctggcc	gcggtcagcc	tggagcgcac	ggtgtgcatc	420
gtgcgcctgc	ggcgcggcct	gagcggcccg	gggcggcgga	cgcaggcggc	gctgctggct	480
ttcatatggg	gttactcggc	gctcgcgcgc	ctgcccctct	gcacattgga	ttggcccaac	540
ccgcagcgcc	ttcccggcgg	ggaccaggaa	attccgattt	gcacattgga	ttggcccaac	600
cgcataggag	aaatctcatg	ggatgtgttt	tttgtgactt	tgaacttcct	ggtaccagga	660
ctggtcattg	tgatcagcta	ctccaagatt	ttacagatca	cgaaagcctc	gcggaagagg	720
cttacgctga	gcttggcata	ctccgagagc	caccagatcc	gagtgtccca	gcaggactac	780
cggctcttcc	gaacgctctt	cctgctcatg	gtttccttct	tcacatgtgt	gagtcccatc	840
atcatcacca	tcctcctcat	cttgatccag	aacttcgggc	aggacctggg	tatctggccg	900
tcccttttct	tctgggtggg	ggccttcacg	tttgccaaact	ccgccctaaa	ccccattctg	960
tacaacatgt	cgctgttcag	gagcgagtgg	aggaagattt	tttgctgctt	ctttttccca	1020
gagaagggag	ccattttttac	agaaacgtct	atcaggcgaa	atgacttgct	tgttatttcc	1080
acc						1083

<210> 10

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<400> 10

gtggtggcct tcacgtttg 19

<210> 11

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<400> 11

cgctcctgaa cagcgacat 19

<210> 12

<211> 26

<212> DNA

<213> Artificial Sequence
 <220>
 <400> 12
 caactccgcc ctaaacccca ttctgt 26
 <210> 13
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <400> 13
 gtcgacatgt cccctgagtg tgcgcagacg acg 33
 <210> 14
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <400> 14
 gctagcttag gtggaaataa cagacaagtc att 33
 <210> 15
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <400> 15
 tccgagtgtc ccaacaagac tac 23
 <210> 16
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <400> 16
 gactccacat gatgaagaag gaaa 24
 <210> 17
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <400> 17
 ccgcacgctc ttctgtctca tg 22
 <210> 18
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <400> 18
 gtggtggcct tcacgtttg 19
 <210> 19
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <400> 19
 cgctcctgaa cagcgacat 19
 <210> 20
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>

<400> 20

caactccgcc ctaaacccca ttctgt

26